

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/512, 737B
Source: IFWP
Date Processed by STIC: 10/10/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/512,737B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|------------------------------------|--|
| 1 | Wrapped Nucleic
Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 | Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. |
| 10 | Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below) |
| 11 | Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules |
| 12 | PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | Misuse of n/Xaa | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid |



IFWP

RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/10/512,737B

TIME: 14:47:03

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J512737B.raw

2 <110> APPLICANT: BioTeSys GmbH
 3 Schelztorstrasse 54-56
 4 D 73728 Esslingen
 5 GERMANY
 W--> 6 <120> TITLE OF INVENTION: transport system in biological systems
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/512,737B
 C--> 7 <141> CURRENT FILING DATE: 2004-10-27
 W--> 0 <130> FILE REFERENCE:
 7 <150> PRIOR APPLICATION NUMBER: A 656/2002
 8 <151> PRIOR FILING DATE: 2002-04-29
 W--> 9 <160> NUMBER OF SEQ ID: 15

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

84 <210> SEQ ID NO: 9
 85 <211> LENGTH: 22
 86 <212> TYPE: PRT
 87 <213> ORGANISM: Artificial sequence
 W--> 88 <220> FEATURE:
 89 <223> OTHER INFORMATION: Amino Acid
 W--> 90 <400> SEQUENCE: 9
 E--> 91 lie Val Ala Ile Leu Ile Cys Ile Leu Ile Leu Leu Thr Met Val Leu Leu Phe Val Met
 E--> 92 Trp Met
 E--> 93 1
 E--> 94 20

Invalid Response.
 What is the source of genetic material? See gleim 11 on summary sheet.

Invalid Amino Acid designator.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/512,737B

DATE: 10/10/2006
TIME: 14:47:05

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\10102006\J512737B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 91,93

Seq#:11; Line(s) 112

VERIFICATION SUMMARY

DATE: 10/10/2006

PATENT APPLICATION: US/10/512,737B

TIME: 14:47:05

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J512737B.raw

L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:14 M:283 W: Missing Blank Line separator, <220> field identifier
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:42 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:283 W: Missing Blank Line separator, <220> field identifier
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:88 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:283 W: Missing Blank Line separator, <400> field identifier
L:91 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:92 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <220> field identifier
L:110 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:283 W: Missing Blank Line separator, <220> field identifier
L:119 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:135 M:283 W: Missing Blank Line separator, <220> field identifier
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:144 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:283 W: Missing Blank Line separator, <400> field identifier